

ABSTRACT

[0057] The present invention relates to a method for measuring the amount of a target nucleic acid in a sample using a standard which is designed to have one base difference compared with the gene of interest or a “target nucleic acid sequence.” Use of such standard in combination with a method of “enhancing” the difference in the standard and the test nucleic acid sample using, for example, a base extension reaction carried right at the mutation site allowing amplification of the standard and target nucleic acids with the same efficiency and facilitating quantification of the target nucleic acid. Thereafter a means of quantifying the “enhanced” standard and target nucleic acid samples is used to determine the amount of the target nucleic acid. In the preferred embodiment, the quantification means is Mass Spectrometry.